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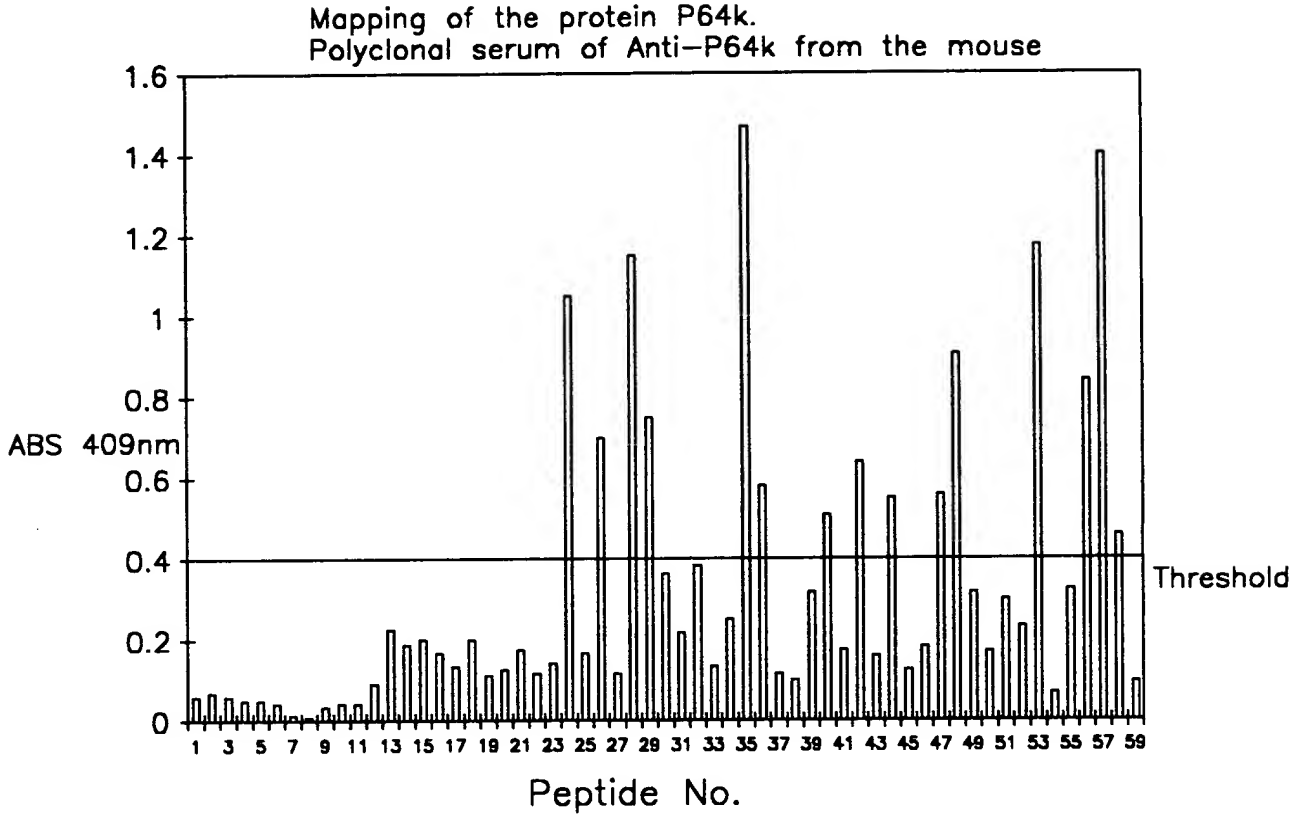
FIG. 1

```
        10         20         30         40         50         60         70
ATGCTAGATA AAAGAATGGC TTTAGTTGAA TTGAAAGTGC CCGACATTGG CGGACACGAA AATGTAGATA
        80         90        100        110        120        130        140
TTATCGCGGT TGAAGTAAAC GTGGGCGACA CTATTGCTGT GGACGATACC CTGATTACTT TGGAAACCGA
       150        160        170        180        190        200        210
TAAAGCGACT ATGGACGTAC CTGCTGAAGT TGCAGGCGTA GTCAAAGAAG TTAAAGTTAA AGTCGGCGAC
       220        230        240        250        260        270        280
AAAATCTCTG AAGGTGGTTT GATTGTCGTC GTTGAAGCTG AAGGCACGGC AGCCGCTCCT AAAGCCGAAG
       290        300        310        320        330        340        350
CGGCTGCCGC CCCGGCGCAA GAAGCCCCTA AAGCTGCCGC TCCTGCTCCG CAAGCCGCGC AATTCGGCGG
       360        370        380        390        400        410        420
TTCTGCCGAT GCCGAGTACG ACGTGGTCGT ATTGGGTGGC GGTCCCGGCG GTTACTCCGC TGCATTTGCC
       430        440        450        460        470        480        490
GCTGCCGATG AAGGCTTGAA AGTCGCCATC GTCGAACGTT ACAAAACTTT GGGCGGCGTT TGCCTGAACG
       500        510        520        530        540        550        560
TCGGCTGTAT CCCTTCCAAA GCCTTGTTGC ACAATGCCGC CGTTATCGAC GAAGTGCGCC ACTTGGCTGC
       570        580        590        600        610        620        630
CAACGGTATC AAATACCCCG AGCCGGAACT CGACATCGAT ATGCTTCGCG CCTACAAAGA CGGCGTAGTT
       640        650        660        670        680        690        700
TCCCGCCTCA CGGGCGGTTT GGCAGGTATG GCGAAAAGCC GTAAAGTGGA CGTTATCCAA GGCGACGGGC
       710        720        730        740        750        760        770
AATTCTTAGA TCCGCACCAC TTGGAAGTGT CGCTGACTGC CGGCGACGCG TACGAACAGG CAGCCCCTAC
       780        790        800        810        820        830        840
CGGCGAGAAA AAAATCGTTG CCTTCAAAAA CTGTATCATT GCAGCAGGCA GCCGCGTAAC CAAACTGCCT
       850        860        870        880        890        900        910
TTCATTCCTG AAGATCCGCA CATCATCGAT TCCAGCGGCG CATTGGCTCT GAAAGAAGTA CCGGGCAAAC
       920        930        940        950        960        970        980
TGCTGATTAT CGGCGGCGGC ATTATCAGCC TCGAGATGGG TACGGTTTAC AGCACGCTGG GTTCGCGTTT
       990       1000       1010       1020       1030       1040       1050
GGATGTGGTT GAAATGATGG ACGGCCTGAT GCAAGGCGCA GACCGCGATT TGGTAAAAGT ATGGCAAAAA
      1060       1070       1080       1090       1100       1110       1120
CAAAACGAAT ACCGTTTTGA CAACATTATG GTCAACACCA AAACCGTTGC AGTTGAGCCG AAAGAAGACG
      1130       1140       1150       1160       1170       1180       1190
GCGTTTACGT TACCTTTGAA GGCGCGAACG CGCCTAAAGA GCCGCAACGC TACGATGCCG TATTGGTTGC
      1200       1210       1220       1230       1240       1250       1260
CGCCGGCCGC GCGCCCAACG GCAAACTCAT CAGCGCGGAA AAAGCAGGCG TTGCCGTAAC CGATCGCGGC
      1270       1280       1290       1300       1310       1320       1330
TTCATCGAAG TGGACAAACA AATGCGTACC AATGTGCCGC ACATCTACGC CATCGGCGAC ATCGTCGGTC
      1340       1350       1360       1370       1380       1390       1400
AGCCGATGTT GGCGCACAAA GCCGTTCACG AAGGCCACGT TGCCGCCGAA AACTGCGCCG GCCACAAAGC
      1410       1420       1430       1440       1450       1460       1470
CTACTTCGAC GCACGCGTGA TTCCGGGCGT TGCCTACACT TCCCCCGAAG TGGCGTGGGT GGGCGAAACC
      1480       1490       1500       1510       1520       1530       1540
GAACTGTCCG CCAAAGCCTC CGGCCGCAAA ATCACCAAAG CCAACTTCCC GTGGGCGGCT TCCGGCCGTG
      1550       1560       1570       1580       1590       1600       1610
CGATTGCCAA CGGTTGCGAC AACGGCTTTA CCAAGCTGAT TTTTGATGCC GAAACCGGCC GCATCATCGG
      1620       1630       1640       1650       1660       1670       1680
CGGCGGCATT GTCGGTCCGA ACGGTGGCGA TATGATCGGC GAAGTCTGCC TTGCCATCGA AATGGGCTGC
      1690       1700       1710       1720       1730       1740       1750
GACGCGGCAG ACATCGGCAA AACCATCCAC CCGCACCCGA CCTTGGGCGA ATCCATCGGT ATGGCGGCGG
      1760       1770       1780       1790       1797
AAGTGGCATT GGGTACTTGT ACCGACCTGC CTCCGCAAAA GAAAAAA
```

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 2



APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 3

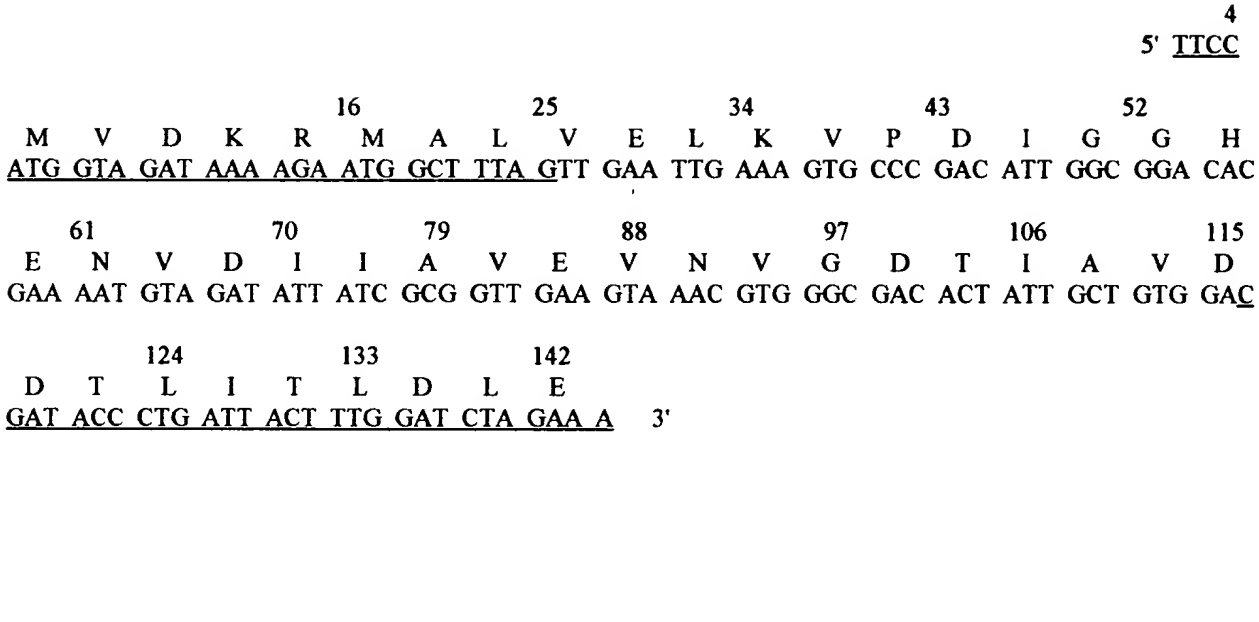


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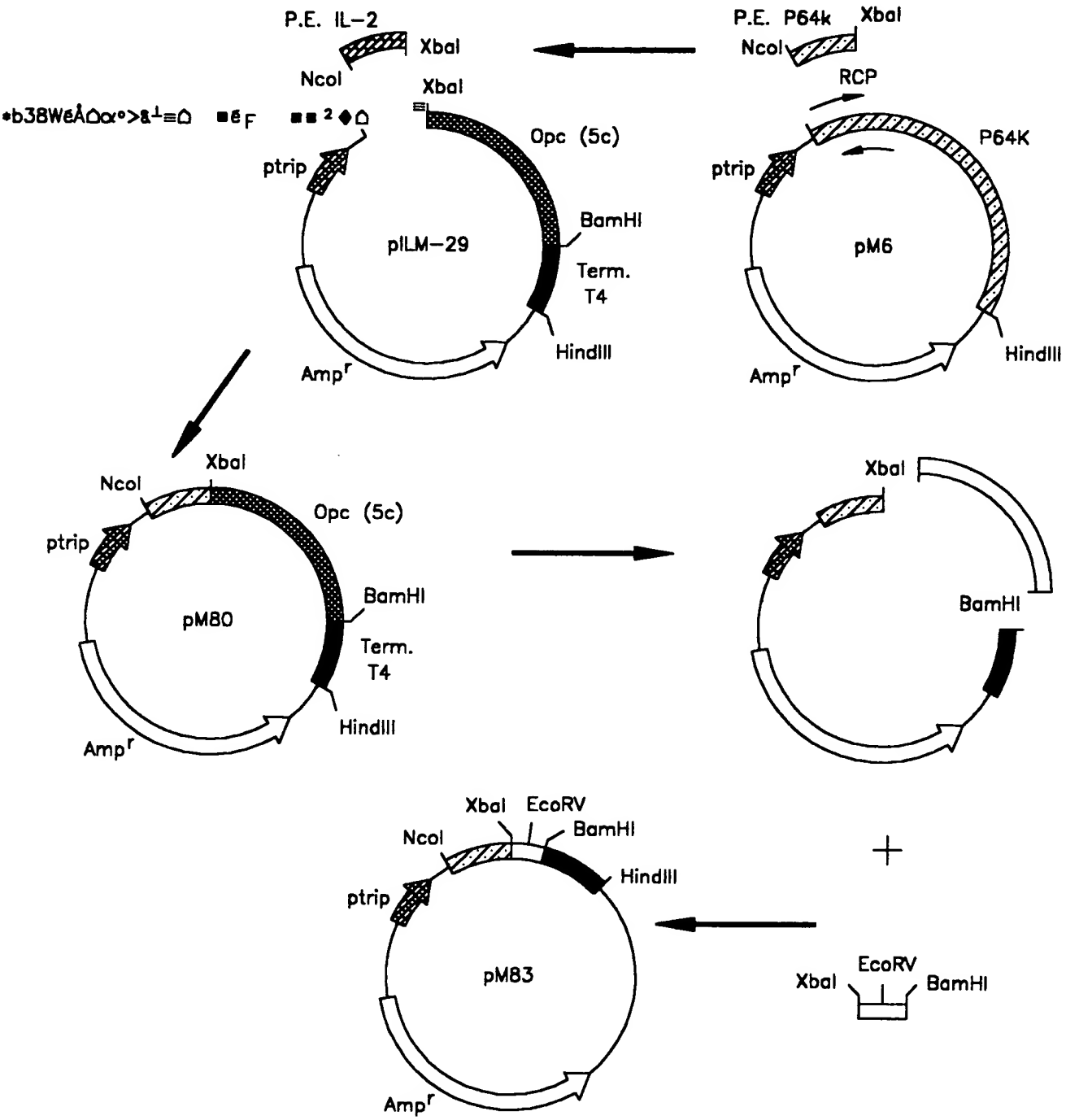
FIG. 4



APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 5

Seqences producing High-scoring Segment Pairs:	High Score	Smallest Poisson Probability P(N)	N
KPY1_HUMAN PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1...	51	0.98	1
KPY1_RAT PYRUVATE KINAZE, M1 (MUSCLE) ISOZYME (EC 2.7.1...	51	0.98	1
KPY2_HUMAN PYRUVATE KINAZE, M2 ISOZYME (EC 2.7.1.40).	51	0.98	1
KPY2_RAT PYRUVATE KINAZE, M2 ISOZYME (EC 2.7.1.40).	51	0.98	1

>KPY1_HUMAN PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40) (CYTOSOLIC THYROID HORMONE-BINDING PROTEIN)
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY1_RAT PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY2_HUMAN PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY2_RAT PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

APPROVED BY EXAMINER O.G. FIG. CLASS SUBCLASS

FIG. 6

Seqences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Poisson Probability P(N)	N
CFMUCIN	Canis familiaris (clone pCTM-A) mucin c-term...	-2	62	0.30	1
HS8671	EST02755 Homo sapiens cDNA clone HFBCA72 sim...	-2	61	0.40	1

>CFMUCIN Canis familiaris (clone pCTM-A) mucin c-terminus RNA, 3' end.
Length = 1733

```
Query:      8 LVELKVPDIGGHENVDIIAVEVNVGDTIAVDD 39
              L E+ VPD   H  V+++A  E+ +G+++  VDD
Sbjct:   1015 LREVQVPDRKLHKGVQLLAGELGIGEALQVDD 920
```

>HS8671 EST02755 Homo sapiens cDNA clone HFBCA72 similar to Mucin CTM-A.
Length = 286

```
Query:      8 LVELKVPDIGGHENVDIIAVEVNVGDTIAVDD 39
              L E+ VPD   HE V++++ E+ VG   VDD
Sbjct:    240 LREVQVPDRKLHEGVQLLSGELGVGKXFQVDD 145
```

Docket # 2001-0010

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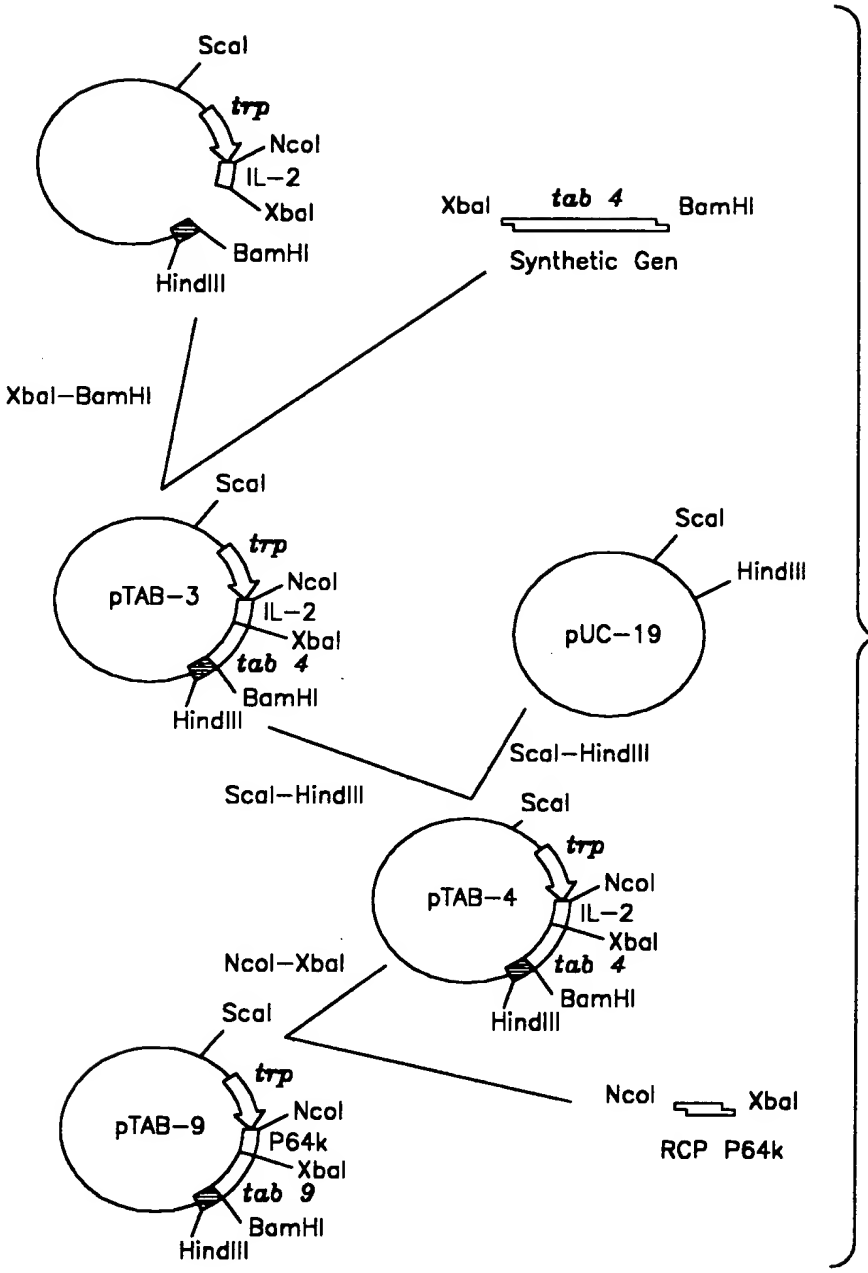


FIG. 7

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 8

```
                12                  21                  30                  39                  48                  57
 M  V  D  K  R  M  A  L  V  E  L  K  V  P  D  I  G  G  H
ATG GTA GAT AAA AGA ATG GCT TTA GTT GAA TTG AAA GTG CCC GAC ATT GGC GGA CAC
                69                  78                  87                  96                  105                 114
 E  N  V  D  I  I  A  V  E  V  N  V  G  D  T  I  A  V  D
AA  AAT GTA GAT ATT ATC GCG GTT GAA GTA AAC GTG GGC GAC ACT ATT GCT GTG GAC
                126                 135                 144                 153                 162                 171
 D  T  L  I  T  L  D  L  D  S  R  G  I  R  I  G  P  G  R
GAT ACC CTG ATT ACT TTG GAT CTA GAC TCG AGA GGC ATT CGT ATC GGC CCA GGT CGC
                183                 192                 201                 210                 219                 228
 A  I  L  A  T  A  G  G  G  A  R  Q  S  T  P  I  G  L  G
GCA ATT TTA GCA ACA GCT GGC GGT GGC GCA CGT CAA TCT ACC CCT ATT GGT TTA GGT
                240                 249                 258                 267                 276                 285
 G  A  L  Y  T  T  A  G  G  G  A  R  K  S  I  T  K  G  P
CAG GCT CTG TAT ACG ACT GCC GGC GGT GGT GCG CGC AAA AGT ATC ACC AAG GGT CCA
                297                 306                 315                 324                 333                 342
 G  R  V  I  Y  A  T  A  G  G  G  A  R  K  R  I  H  I  G
GGC CGC GTC ATT TAC GCC ACC GCG GGC GGC GGT GCC CGT AAG CGT ATC CAC ATT GGC
                354                 363                 372                 381                 390                 399
 P  G  R  A  F  Y  T  T  A  G  G  G  A  R  K  R  I  T  M
CCA GGC CGT GCA TTC TAT ACT ACA GCA GGT GGT GGC GCA CGT AAA CGC ATC ACT ATG
                411                 420                 429                 438                 447                 456
 G  P  G  R  V  Y  Y  T  T  A  G  G  G  A  S  I  R  I  Q
GGT CCT GGT CGC GTC TAT TAC ACG ACC GCT GGC GGC GGT GCT AGC ATT CGC ATC CAA
                468                 477                 486                 495
 R  G  P  G  R  A  F  V  T  I  *
CGC GGC CCT GGT CGT GCA TTT GTG ACC ATA TGA
```

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 9A

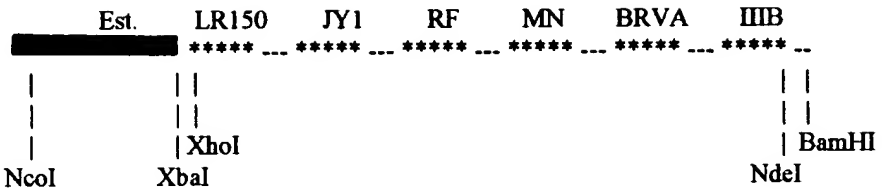
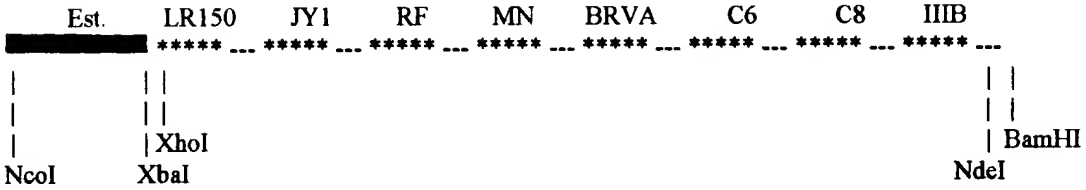


FIG. 9B



APPROVED O.G. FIG.
BY CLASS SUBCLASS

FIG. 10A

Gene	Stabilizer	Plasmid	Culture medium	% of expression
porA	hIL2-58	pILM-28	M9	32
	P64k-47	pM-82	M9	34
opc	hIL2-58	pILM-29	M9	25
	P64k-47	pM-80	M9	20
TAB	hIL2-22	pTAB4	LB	5
	P64k-47	pTAB4	LB	10

FIG. 10B

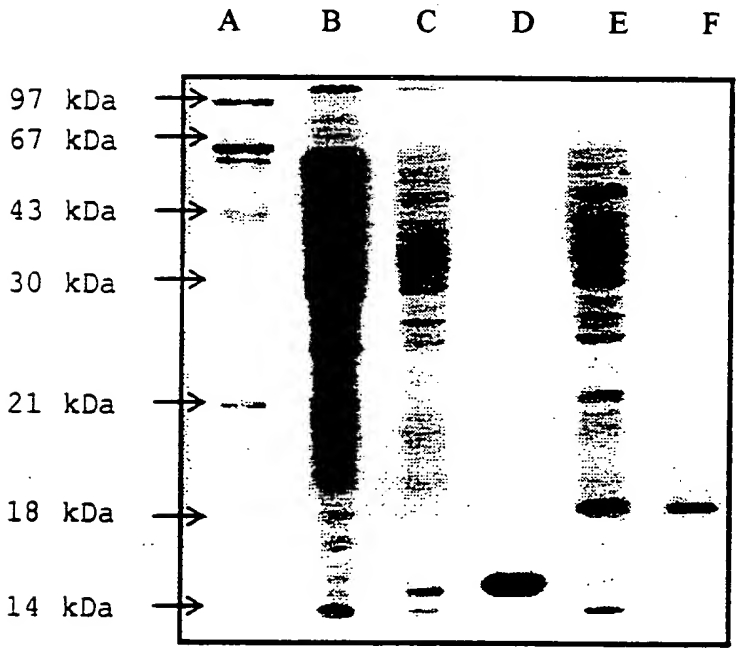
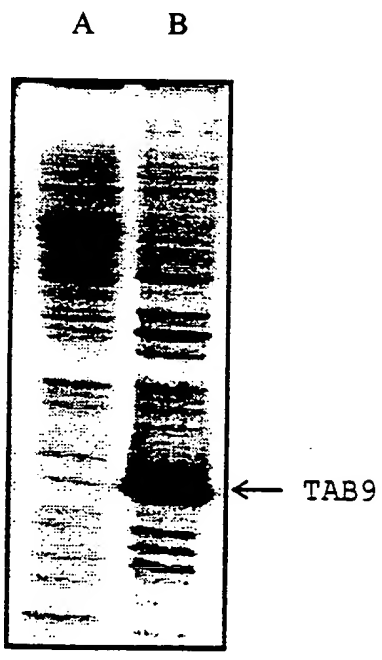
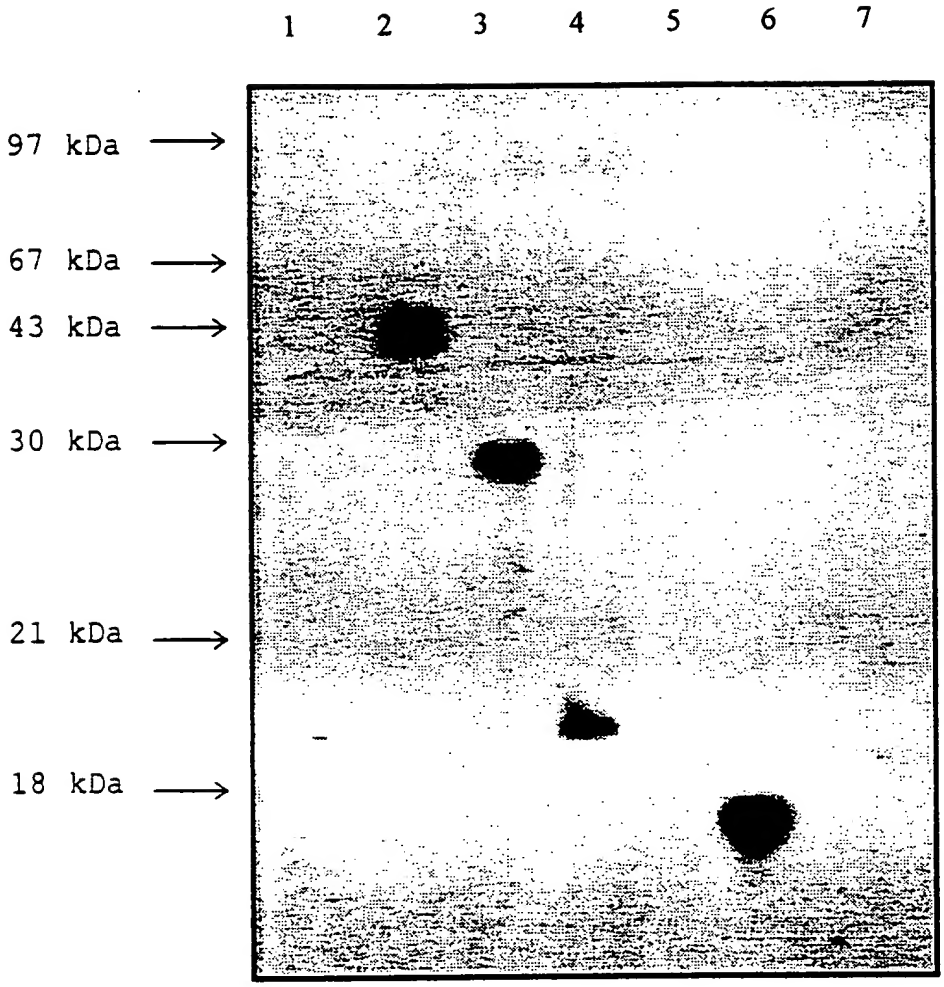


FIG. 10C



APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 11



APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 12

	TAB 4				TAB 9			
RABBIT#	12166	5725	5340	2310	1	2	3	10
TAB	20480	10240	10240	81920	20480	20480	51200	51200
	0	0	0	0	0	0		
LR150	<100	<100	<100	6400	400	<100	800	<100
JY1	200	<100	<100	12800	1600	6400	3200	<100
RF	6400	<100	3200	800	<100	200	3200	800
MN	200	<100	<100	1600	1600	3200	6400	<100
BRVA	<100	6400	400	3200	800	400	6400	1600
IIIB	<100	<100	<100	<100	800	<100	800	<100
GM	1820				1416			
R%	45.8%				75%			

0054250.0050